AMENDMENTS TO THE CLAIMS:

Please replace the claims with the claims provided in the listing below

wherein status, amendments, additions and cancellations are indicated.

1.   (Currently amended)   ~~A method~~ Method for recording sequence information

on biological compounds, comprising the steps of:

dividing [[the]] one of text data representing [[the]] a sequence of said

biological compounds ~~or the~~ and numerical data obtained by converting said text

data ~~based on,~~ utilizing a conversion rule, into a plurality of m-bit partial data

arranged in a plurality of columns in [[the]] an arranged direction corresponding

to [[the]] a direction along which said biological compounds are placed and in a

plurality of rows in [[the]] a non-arranged direction which crosses said arranged

direction, where m is an integer ~~larger~~ greater than or equal to 16;

computing a first set of parity information by applying a first operation of

a Galois field GF(2^m) along said non-arranged direction to a set of said partial data

of each column;

computing a second set of parity information by applying a second operation

of a Galois field GF(2^m) along said arranged direction to a set of said partial data

of each row; and

representing said sequence information on said biological compounds by

said first and second sets of parity information.

2.   (Currently amended)   ~~The method~~ Method of claim 1, wherein

~~assuming that~~ when α is a primitive element of $\underline{a}$ Galois field $GF(2^m)$,

said first set of parity information includes [[the]] $\underline{a}$ sum of a plurality of

products obtained by multiplying a set of said partial data of each column along

said non-arranged direction by α^{sp}, $\alpha^{s(p+1)}$, $\alpha^{s(p+2)}$, ...,$\alpha^{s(p+dp)}$, where s and p are

nonnegative integers and dp is an integer ~~lager~~ greater than or equal to one; and

said second set of parity information includes [[the]] $\underline{a}$ sum of a plurality

of products obtained by multiplying a set of said partial data of each row along said

arranged direction by α^{tq}, $\alpha^{t(q+1)}$, $\alpha^{t(q+2)}$, ..., $\alpha^{t(q+dq)}$, where t and q are nonnegative

integers and dq is an integer ~~lager~~ greater than or equal to one.

3.   (Currently amended)   ~~The method~~ Method of claim 2, wherein

[[the]] $\underline{a}$ number of said partial data placed along said arranged direction

is smaller than [[the]] $\underline{a}$ number of said partial data placed along said non-arranged

direction; and

[[the]] $\underline{a}$ number of said second set of parity information is smaller than

[[the]] $\underline{a}$ number of said first set of parity information.

4.   (Currently amended)   ~~The method~~ Method of claim 3, wherein [[the]] said

number of said partial data placed along said non-arranged direction is ~~smaller~~ less

than or equal to $(2^m-1)/4$.

5.   (Currently amended)   ~~The method~~ Method of claim 2, wherein both of

said integers s and t are zero.

6.   (Currently amended)   ~~The method~~ Method of claim 2, wherein both of

said integers s and t are one.

7.   (Currently amended)   ~~The method~~ Method of claim 2, wherein

said first set of parity information includes a plurality of said sums

obtained for each column using mutually different values of said integer s; and

said second set of parity information includes a plurality of said sums

obtained for each row using mutually different values of said integer t.

8.   (Currently amended)   ~~The method~~ Method of claim 1, wherein said partial

data is said numerical data obtained by expressing each of said biological

compounds [[in]] as data ~~whose~~ having a size [[is]] less than or equal to six bits.

9.   (Currently amended)   ~~The method~~ Method of claim 1, wherein said integer

m that defines <u>said</u> Galois field GF(2^m) is a multiple of 64.

10.   (Currently amended)   ~~The method~~ Method of claim 1, further ~~including~~

<u>comprising</u> the steps of:

  ~~assuming~~ <u>making an assumption</u> that said sequence of said biological

compounds is a standard sequence;

  computing two sets of parity information on a sequence of biological

compounds subject to examination ~~correspondingly~~, <u>said two sets of parity</u>

<u>information on said sequence of biological compounds subject to examination</u>

<u>corresponding</u> to said two sets of parity information on said standard sequence; and

  identifying [[the]] differences between said standard sequence and said

sequence of biological compounds subject to examination<u>,</u> by using said [[four]]

<u>two</u> sets of parity information <u>on said standard sequence and said two sets of parity</u>

<u>information on said sequence of biological compounds subject to examination</u>.

11.   (Currently amended)   ~~The method~~ Method of claim 1, wherein said

biological compounds are nucleotides constituting at least part of DNA, RNA, or

a gene.

12.   (Currently amended)   ~~The method~~ Method of claim 1, wherein said

biological compounds are amino acids constituting at least part of a protein.

13.   (Currently amended)   ~~A device~~ Device for recording sequence information

on biological compounds, comprising:

a sequencer for reading sequence information on said

biological compounds;

dividing means for dividing [[the]] one of text data

representing [[the]] a sequence of said biological compounds ~~or the~~ and numerical

data obtained by converting said text data ~~based on~~ utilizing a conversion rule, into

a plurality of m-bit partial data arranged in a plurality of columns in [[the]] an

arranged direction corresponding to [[the]] a direction along which said biological

compounds are placed, and in a plurality of rows in [[the]] a non-arranged direction

which crosses said arranged direction, where m is an integer ~~larger~~ greater than or

equal to 16;

computing means for computing a first set of parity information by applying

a first operation of a Galois field $GF(2^m)$ along said non-arranged direction to a set

of said partial data of each column and computing a second set of parity

information by applying a second operation of a Galois field $GF(2^m)$ along said

arranged direction to a set of said partial data of each row; and

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recording means for recording said first and second sets of parity information in a recording medium.

14.   (Currently amended)   ~~The device~~ Device of claim 13, wherein

~~assuming that~~ when α is a primitive element of a Galois field GF(2^m),

said first set of parity information includes [[the]] a sum of a plurality of products obtained by multiplying a set of said partial data of each column along said non-arranged direction by α^{sp}, $\alpha^{s(p+1)}$, $\alpha^{s(p+2)}$, ...,$\alpha^{s(p+dp)}$, where s and p are nonnegative integers and dp is an integer ~~lager~~ greater than or equal to one; and

said second set of parity information includes [[the]] a sum of a plurality of products obtained by multiplying a set of said partial data of each row along said arranged direction by α^{tq}, $\alpha^{t(q+1)}$, $\alpha^{t(q+2)}$, ..., $\alpha^{t(q+dq)}$, where t and q are nonnegative integers and dq is an integer ~~lager~~ greater than or equal to one.

15.   (Currently amended)   ~~A computer-readable~~ Computer-readable medium for storing sequence information on biological compounds, comprising:

a data structure stored in said medium, wherein ~~in order to~~

~~form said data structure~~,

[[the]] one of text data representing [[the]] a sequence of said biological compounds ~~or the~~ and numerical data obtained by converting said text data ~~based~~

on utilizing a conversion rule is divided into a plurality of m-bit partial data arranged in a plurality of columns in [[the]] an arranged direction, corresponding to [[the]] a direction along which said biological compounds are placed, and in a plurality of rows in [[the]] a non-arranged direction which crosses said arranged direction, where m is an integer larger greater than or equal to 16;

a first set of parity information is computed by applying a first operation of a Galois field $GF(2^m)$ along said non-arranged direction to a set of said partial data of each column and a second set of parity information is computed by applying a second operation of a Galois field $GF(2^m)$ along said arranged direction to a set of said partial data of each row; and

said first and second sets of parity information are recorded in said data structure as said sequence information on said biological compounds.

16.   (Currently amended)   The computer-readable Computer-readable medium of claim 15, wherein

said data structure further includes a mathematical digest of one of said text data representing said sequence of said biological compounds [[or]] and said numerical data corresponding to said text data, where and

the size of said mathematical digest is larger has a size greater than or equal to 40 bits.

17.   (Currently amended)   ~~A method~~ Method for supplying sequence information on biological compounds, comprising the steps of:

~~as the procedure of a supplier,~~

recording [[the]] one of text data representing [[the]] a sequence of said biological compounds ~~or the~~ and numerical data obtained by converting said text data ~~based on~~ utilizing a conversion rule, in a first file;

dividing said one of text data and numerical data recorded in said first file ~~or said numerical data recorded in said first file~~ into a plurality of m-bit partial data arranged in a plurality of columns in [[the]] an arranged direction corresponding to [[the]] a direction along which said biological compounds are placed, and in a plurality of rows in [[the]] a non-arranged direction which crosses said arranged direction, where m is an integer ~~larger~~ greater than or equal to 16;

computing a first set of parity information by applying a first operation of a Galois field $GF(2^m)$ along said non-arranged direction to a set of said partial data of each column, and computing a second set of parity information by applying a second operation of a Galois field $GF(2^m)$ along said arranged direction to a set of said partial data of each row;

recording said first and second sets of parity information in a second file; and

~~as the procedure of a user,~~

~~receiving~~ providing said two sets of parity information recorded in said

second file through a communications network ~~from said supplier~~.

18.   (Currently amended)   ~~The method of claim 17, further including~~ Method

for utilizing sequence information on biological compounds, comprising the steps

of:

~~as the procedure of said user,~~ receiving through said communications network

from a supplier said two sets of parity information recorded on said second file,

according to claims 17;

identifying [[the]] differences between said sequence of said biological

compounds held by said supplier and [[the]] a sequence of biological compounds

subject to examination, based on said two sets of received parity information; and

when said differences cannot be recovered, ~~said user~~ receiving [[the]]

sequence information on [[the]] a part corresponding to said differences, within

said one of text data and numerical data recorded in said first file ~~or said numerical~~

~~data recorded in said first file,~~ through said communications network from said

supplier.

19.   (Currently amended)   ~~The method~~ Method of claim 18, wherein

~~assuming that~~ <u>when</u> α is a primitive element of <u>a</u> Galois field GF(2^m),

said first set of parity information includes [[the]] <u>a</u> sum of a plurality of products obtained by multiplying a set of said partial data of each column along said non-arranged direction by α^{sp}, $\alpha^{s(p+1)}$, $\alpha^{s(p+2)}$, ..., $\alpha^{s(p+dp)}$, where s and p are nonnegative integers and dp is an integer ~~lager~~ <u>greater</u> than or equal to one; and

said second set of parity information includes [[the]] <u>a</u> sum of a plurality of products obtained by multiplying a set of said partial data of each row along said arranged direction by α^{tq}, $\alpha^{t(q+1)}$, $\alpha^{t(q+2)}$, ..., $\alpha^{t(q+dq)}$, where t and q are nonnegative integers and dq is an integer ~~lager~~ <u>greater</u> than or equal to one.

20.   (Currently amended)   ~~The method~~ <u>Method</u> of claim [[18]] <u>17</u>, further ~~including~~ <u>comprising</u> the ~~steps~~ <u>step</u> of:

~~as the procedure of said supplier,~~

~~letting the~~ <u>providing</u> information on [[the]] <u>a</u> number of said sequence of said biological compounds<u>,</u> and [[the]] information on a mathematical digest of said <u>one</u> <u>of</u> text data ~~or said~~ <u>and</u> numerical data ~~be disclosed to the public~~ through said communications network<u>;</u> ~~and~~

~~as the procedure of a user,~~

~~accessing said information on the number of said sequence of biological compounds and said information on said mathematical digest through said communications network before receiving said two sets of parity information.~~

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21.   (Currently amended)   ~~A method~~ Method for recording sequence information on biological compounds, comprising the steps of:

dividing [[the]] one of text data representing [[the]] a sequence of said biological compounds ~~or the~~ and numerical data obtained by converting said text data ~~based on~~ utilizing a conversion rule, into a plurality of m-bit partial data arranged in a plurality of columns in [[the]] an arranged direction corresponding to [[the]] a direction along which said biological compounds are placed, and in a plurality of rows in [[the]] a non-arranged direction which crosses said arranged direction, where m is an integer ~~larger~~ greater than or equal to 16;

~~assuming~~ making assumptions that a maximum value of said partial data is Nmax, and a prime number larger than said maximum value Nmax is P;

computing a first set of parity information by applying a first operation of a Galois field GF(P) along said non-arranged direction to a set of said partial data of each column;

computing a second set of parity information by applying a second operation of a Galois field GF(P) along said arranged direction to a set of said partial data of each row; and

representing said sequence information on said biological compounds by said first and second sets of parity information.

22. (Currently amended) ~~The method~~ <u>Method</u> of claim 21, wherein

said maximum value Nmax of said partial data is smaller than $(2^m - 1)$ and

said prime number P satisfies the following condition:

$2^m > P > \text{Nmax}$.

23. (Currently amended) ~~The method~~ <u>Method</u> of claim 22, wherein

~~assuming that~~ <u>when</u> δ is a primitive element of <u>a</u> Galois field GF(P),

said first set of parity information includes [[the]] <u>a</u> sum of a plurality of

products obtained by multiplying a set of said partial data of each column along

said non-arranged direction by δ^{sp}, $\delta^{s(p+1)}$, $\delta^{s(p+2)}$, ..., $\delta^{s(p+dp)}$, where s and p are

nonnegative integers and dp is an integer ~~lager~~ <u>greater</u> than or equal to one; and

said second set of parity information includes [[the]] <u>a</u> sum of a plurality

of products obtained by multiplying a set of said partial data of each row along said

arranged direction by δ^{tq}, $\delta^{t(q+1)}$, $\delta^{t(q+2)}$, ..., $\delta^{t(q+dq)}$, where t and q are nonnegative

integers and dq is an integer ~~lager~~ <u>greater</u> than or equal to one.

24. (Currently amended) ~~A method~~ <u>Method</u> for supplying sequence

information on biological compounds, comprising the steps of:

~~as the procedure of a supplier,~~

recording [[the]] <u>one of</u> text data representing the sequence of said

biological compounds ~~or the~~ and numerical data obtained by converting said text

data ~~based on~~ utilizing a conversion rule, in a first file;

dividing said one of said text data and said numerical data recorded in said

first file ~~or said numerical data recorded in said first file~~ into a plurality of m-bit

partial data arranged in a plurality of columns in [[the]] an arranged direction

corresponding to [[the]] a direction along which said biological compounds are

placed, and in a plurality of rows in [[the]] a non-arranged direction which crosses

said arranged direction, where m is an integer larger than or equal to 16;

~~assuming~~ making assumptions that a maximum value of said partial data

is Nmax, and a prime number larger than said maximum value Nmax is P;

computing a first set of parity information by applying a first operation of

a Galois field GF(P) along said non-arranged direction to a set of said partial data

of each column and computing a second set of parity information by applying a

second operation of a Galois field GF(P) along said arranged direction to a set of

said partial data of each row;

recording said first and second sets of parity information in a second file;

and

~~as the procedure of a user,~~

~~receiving~~ providing said two sets of parity information recorded in said second

file through a communications network ~~from said supplier~~.

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25.   (Currently amended)   ~~The method of claim 24, further including~~ Method for utilizing

sequence information on biological compounds comprising the steps of:

~~as the procedure of said user,~~ receiving through said communications network from a

supplier said two sets of parity information recorded in said second file, according to claim

24;

identifying [[the]] differences between said sequence of said biological compounds

held by said supplier and [[the]] a sequence of biological compounds subject to

examination, based on said two sets of received parity information and

when said differences cannot be recovered, ~~said user~~ receiving [[the]] sequence

information on [[the]] a part corresponding to said differences, within said one of text data

recorded in said first file ~~or said numerical data recorded in said first file,~~ through said

communications network from said supplier

26.   (New) Method of claim 18, further comprising the step of:

accessing at least one of information on a number of said sequence of said

biological compounds, and information on a mathematical digest of said one of text data

and numerical data, through said communications network.

CLAIMS

What is claimed is:

5   1. A method for recording sequence information on biological compounds, comprising the steps of:

dividing the text data representing the sequence of said biological compounds or the numerical data obtained by converting said text data based on a conversion rule into a plurality of m-bit partial data arranged in a plurality of

10   columns in the arranged direction corresponding to the direction along which said biological compounds are placed and in a plurality of rows in the non-arranged direction which crosses said arranged direction, where m is an integer larger than or equal to 16;

computing a first set of parity information by applying a first

15   operation of Galois field $GF(2^m)$ along said non-arranged direction to a set of said partial data of each column;

computing a second set of parity information by applying a second operation of Galois field $GF(2^m)$ along said arranged direction to a set of said partial data of each row; and

20   representing said sequence information on said biological compounds by said first and second sets of parity information.

2. The method of claim 1, wherein

assuming that α is a primitive element of Galois field $GF(2^m)$,

25   said first set of parity information includes the sum of a plurality of products obtained by multiplying a set of said partial data of each column along said non-arranged direction by α^{sp}, $\alpha^{s(p+1)}$, $\alpha^{s(p+2)}$, $\cdots$, $\alpha^{s(p+dp)}$, where s and p are nonnegative integers and dp is an integer lager than or equal to one; and

said second set of parity information includes the sum of a plurality of

30   products obtained by multiplying a set of said partial data of each row along said arranged direction by α^{tq}, $\alpha^{t(q+1)}$, $\alpha^{t(q+2)}$, $\cdots$, $\alpha^{t(q+dq)}$, where t and q are nonnegative integers and dq is an integer lager than or equal to one.

3. The method of claim 2, wherein

the number of said partial data placed along said arranged direction is smaller than the number of said partial data placed along said non-arranged direction; and

the number of said second set of parity information is smaller than the

5 number of said first set of parity information.

4. The method of claim 3, wherein the number of said partial data placed along said non-arranged direction is smaller than or equal to $(2^m-1)/4$.

10 5. The method of claim 2, wherein both of said integers s and t are zero.

6. The method of claim 2, wherein both of said integers s and t are one.

7. The method of claim 2, wherein

15 said first set of parity information includes a plurality of said sums obtained for each column using mutually different values of said integer s; and

said second set of parity information includes a plurality of said sums obtained for each row using mutually different values of said integer t.

20 8. The method of claim 1, wherein said partial data is said numerical data obtained by expressing each of said biological compounds in data whose size is less than or equal to six bits.

9. The method of claim 1, wherein said integer m that defines Galois field $GF(2^m)$ is

25 a multiple of 64.

10. The method of claim 1, further including the steps of:

assuming that said sequence of said biological compounds is a standard sequence;

30 computing two sets of parity information on a sequence of biological compounds subject to examination correspondingly to said two sets of parity information on said standard sequence; and

identifying the differences between said standard sequence and said sequence of biological compounds subject to examination by using said four sets of

parity information.

11. The method of claim 1, wherein said biological compounds are nucleotides constituting at least part of DNA, RNA, or a gene.

12. The method of claim 1, wherein said biological compounds are amino acids constituting at least part of a protein.

13. A device for recording sequence information on biological compounds, comprising:

a sequencer for reading sequence information on said biological compounds;

dividing means for dividing the text data representing the sequence of said biological compounds or the numerical data obtained by converting said text data based on a conversion rule into a plurality of m-bit partial data arranged in a plurality of columns in the arranged direction corresponding to the direction along which said biological compounds are placed and in a plurality of rows in the non-arranged direction which crosses said arranged direction, where m is an integer larger than or equal to 16;

computing means for computing a first set of parity information by applying a first operation of Galois field $GF(2^m)$ along said non-arranged direction to a set of said partial data of each column and computing a second set of parity information by applying a second operation of Galois field $GF(2^m)$ along said arranged direction to a set of said partial data of each row; and

recording means for recording said first and second sets of parity information in a recording medium.

14. The device of claim 13, wherein

assuming that α is a primitive element of Galois field $GF(2^m)$,

said first set of parity information includes the sum of a plurality of products obtained by multiplying a set of said partial data of each column along said non-arranged direction by α^{sp}, $\alpha^{s(p+1)}$, $\alpha^{s(p+2)}$, $\cdots$, $\alpha^{s(p+dp)}$, where s and p are nonnegative integers and dp is an integer lager than or equal to one; and

said second set of parity information includes the sum of a plurality of

products obtained by multiplying a set of said partial data of each row along said arranged direction by α^{tq}, $\alpha^{t(q+1)}$, $\alpha^{t(q+2)}$, $\cdots$, $\alpha^{t(q+dq)}$, where t and q are nonnegative integers and dq is an integer lager than or equal to one.

15. A computer-readable medium storing sequence information on biological compounds, comprising:

a data structure stored in said medium, wherein in order to form said data structure,

the text data representing the sequence of said biological compounds or the numerical data obtained by converting said text data based on a conversion rule is divided into a plurality of m-bit partial data arranged in a plurality of columns in the arranged direction corresponding to the direction along which said biological compounds are placed and in a plurality of rows in the non-arranged direction which crosses said arranged direction, where m is an integer larger than or equal to 16;

a first set of parity information is computed by applying a first operation of Galois field $GF(2^m)$ along said non-arranged direction to a set of said partial data of each column and a second set of parity information is computed by applying a second operation of Galois field $GF(2^m)$ along said arranged direction to a set of said partial data of each row; and

said first and second sets of parity information are recorded in said data structure as said sequence information on said biological compounds.

16. The computer-readable medium of claim 15, wherein

said data structure further includes a mathematical digest of said text data representing said sequence of said biological compounds or said numerical data corresponding to said text data, where

the size of said mathematical digest is larger than or equal to 40 bits.

17. A method for supplying sequence information on biological compounds, comprising the steps of:

as the procedure of a supplier,

recording the text data representing the sequence of said biological compounds or the numerical data obtained by converting said text data based on a conversion rule in a first file;

dividing said text data recorded in said first file or said numerical data recorded in said first file into a plurality of m-bit partial data arranged in a plurality of columns in the arranged direction corresponding to the direction along which said biological compounds are placed and in a plurality of rows in the non-arranged

5   direction which crosses said arranged direction, where m is an integer larger than or equal to 16;

computing a first set of parity information by applying a first operation of Galois field $GF(2^m)$ along said non-arranged direction to a set of said partial data of each column and computing a second set of parity information by applying a second

10   operation of Galois field $GF(2^m)$ along said arranged direction to a set of said partial data of each row;

recording said first and second sets of parity information in a second file; and

as the procedure of a user,

15   receiving said two sets of parity information recorded in said second file through a communications network from said supplier.

18. The method of claim 17, further including the steps of:

as the procedure of said user,

20   identifying the differences between said sequence of said biological compounds held by said supplier and the sequence of biological compounds subject to examination based on said two sets of parity information; and

when said differences cannot be recovered, said user receiving the sequence information on the part corresponding to said differences within said text data

25   recorded in said first file or said numerical data recorded in said first file through said communications network from said supplier.

19. The method of claim 18, wherein

assuming that α is a primitive element of Galois field $GF(2^m)$,

30   said first set of parity information includes the sum of a plurality of products obtained by multiplying a set of said partial data of each column along said non-arranged direction by α^{sp}, $\alpha^{s(p+1)}$, $\alpha^{s(p+2)}$, $\cdots$, $\alpha^{s(p+dp)}$, where s and p are nonnegative integers and dp is an integer lager than or equal to one; and

said second set of parity information includes the sum of a plurality of

products obtained by multiplying a set of said partial data of each row along said arranged direction by α^{tq}, $\alpha^{t(q+1)}$, $\alpha^{t(q+2)}$, $\cdots$, $\alpha^{t(q+dq)}$, where t and q are nonnegative integers and dq is an integer lager than or equal to one.

20. The method of claim 18, further including the steps of:

as the procedure of said supplier,

letting the information on the number of said sequence of said biological compounds and the information on a mathematical digest of said text data or said numerical data be disclosed to the public through said communications network; and

as the procedure of a user,

accessing said information on the number of said sequence of biological compounds and said information on said mathematical digest through said communications network before receiving said two sets of parity information.

21. A method for recording sequence information on biological compounds, comprising the steps of:

dividing the text data representing the sequence of said biological compounds or the numerical data obtained by converting said text data based on a conversion rule into a plurality of m-bit partial data arranged in a plurality of columns in the arranged direction corresponding to the direction along which said biological compounds are placed and in a plurality of rows in the non-arranged direction which crosses said arranged direction, where m is an integer larger than or equal to 16;

assuming that a maximum value of said partial data is Nmax and a prime number larger than said maximum value Nmax is P;

computing a first set of parity information by applying a first operation of Galois field GF(P) along said non-arranged direction to a set of said partial data of each column;

computing a second set of parity information by applying a second operation of Galois field GF(P) along said arranged direction to a set of said partial data of each row; and

representing said sequence information on said biological compounds by said first and second sets of parity information.

22. The method of claim 21, wherein

said maximum value Nmax of said partial data is smaller than $(2^m - 1)$ and said prime number P satisfies the following condition:

$2^m > P > Nmax$.

23. The method of claim 22, wherein

assuming that δ is a primitive element of Galois field GF(P),

said first set of parity information includes the sum of a plurality of products obtained by multiplying a set of said partial data of each column along said non-arranged direction by δ^{sp}, $\delta^{s(p+1)}$, $\delta^{s(p+2)}$, $\cdots$, $\delta^{s(p+dp)}$, where s and p are nonnegative integers and dp is an integer lager than or equal to one; and

said second set of parity information includes the sum of a plurality of products obtained by multiplying a set of said partial data of each row along said arranged direction by δ^{tq}, $\delta^{t(q+1)}$, $\delta^{t(q+2)}$, $\cdots$, $\delta^{t(q+dq)}$, where t and q are nonnegative integers and dq is an integer lager than or equal to one.

24. A method for supplying sequence information on biological compounds, comprising the steps of:

as the procedure of a supplier,

recording the text data representing the sequence of said biological compounds or the numerical data obtained by converting said text data based on a conversion rule in a first file;

dividing said text data recorded in said first file or said numerical data recorded in said first file into a plurality of m-bit partial data arranged in a plurality of columns in the arranged direction corresponding to the direction along which said biological compounds are placed and in a plurality of rows in the non-arranged direction which crosses said arranged direction, where m is an integer larger than or equal to 16;

assuming that a maximum value of said partial data is Nmax and a prime number larger than said maximum value Nmax is P;

computing a first set of parity information by applying a first operation of Galois field GF(P) along said non-arranged direction to a set of said partial data of each column and computing a second set of parity information by applying a second operation of Galois field GF(P) along said arranged direction to a set of said partial

data of each row;

recording said first and second sets of parity information in a second file; and

as the procedure of a user,

5   receiving said two sets of parity information recorded in said second file through a communications network from said supplier.

25. The method of claim 24, further including the steps of:

as the procedure of said user,

10   identifying the differences between said sequence of said biological compounds held by said supplier and the sequence of biological compounds subject to examination based on said two sets of parity information; and

when said differences cannot be recovered, said user receiving the sequence information on the part corresponding to said differences within said text data

15   recorded in said first file or said numerical data recorded in said first file through said communications network from said supplier.